

11420122.APP  
SEQUENCE LISTING

<110> Pausch, Mark H  
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM, AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011  
<141> 1997-03-11

<150> 07/332,312  
<151> 1994-10-31

<150> PCT/US95/14364  
<151> 1995-10-25

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<170> PatentIn Ver. 2.1

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Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu
		50			55				60						
Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro
		65			70			75			80				
Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
		85			90				95						
Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser
		100			105				110						
Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile

115

120

125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe  
 130 135 140

Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met  
 145 150 155 160

Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr  
 165 170 175

Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro  
 180 185 190

Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser  
 195 200 205

Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr  
 210 215 220

Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe  
 225 230 235 240

Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly  
 245 250 255

Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys  
 260 265 270

Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr  
 275 280 285

Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg  
 290 295 300

Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr  
 305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp  
 325 330 335

Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg  
 340 345 350

Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly  
 355 360 365

Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu  
 370 375 380

Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu  
 385 390 395 400

Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu  
 405 410 415

Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser  
 420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr  
 435 440 445

Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu  
 Page 12

450

455

460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu  
 465 470 475 480

Trp

<210> 38  
 <211> 337  
 <212> PRT  
 <213> *Caenorhabditis elegans*

<220>  
 <221> UNSURE  
 <222> (337)  
 <223> X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

<400> 38  
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Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser  
 20 25 30

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn  
 35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser  
 50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly  
 65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys  
 85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His  
 100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile  
 115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val  
 130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser  
 145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly  
 165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu  
 180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe  
 195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val  
 210 215 220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln  
 Page 13

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225	230	235	240
Asp Ala Arg Ser Ala	Leu Ala Val Val	Gly Gly Lys Val Val	Leu Val
245	250	255	
Ser Glu Leu Tyr Ala Asn Leu Met	Gln Lys Arg Ala Arg Asn Met Ser		
260	265	270	
Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile			
275	280	285	
Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr			
290	295	300	
Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln			
305	310	315	320
Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys			
325	330	335	

Xaa

<210> 39  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
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PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>  
<221> variation  
<222> (2)  
<223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39  
tnggatwygg wgaywyt 17

<210> 40  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: DEGENERATE  
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40  
rtcwccrwah ccdaydgt 18

<210> 41  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 41  
cgcaggcaga gccacaaaga gtacacag 28

<210> 42  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 ggagatcagc taggcaccat atttgg

26

<210> 43  
 <211> 26  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
 atgctgcattg cctcatgctt cccagc

26

<210> 44  
 <211> 20  
 <212> DNA  
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<400> 44  
 gtttatttaa agagagggct

20

<210> 45  
 <211> 426  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val  
 1 5 10 15  
 Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys  
 20 25 30  
 Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val  
 35 40 45  
 Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr  
 50 55 60  
 Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe  
 65 70 75 80  
 Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val  
 85 90 95  
 Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr  
 100 105 110  
 Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly  
 115 120 125  
 Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu  
 130 135 140  
 Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe  
 145 150 155 160

11420122.APP

Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile  
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val  
180 185 190

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Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu  
195 200 205

Asp Thr Phe Ile Lys Trp Asn Val Ser Gln Thr Lys Ile Arg Ile Ile  
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu  
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala  
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr  
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val  
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu  
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu  
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val  
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr  
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu  
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu  
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu  
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly  
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys  
420 425

<210> 46  
<211> 2130  
<212> DNA  
<213> Homo sapiens

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<221> unsure  
<222> (35)  
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NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2057)  
 <223> N AT POSITION 2057 INDICATES UNDETERMINED  
 NUCLEOTIDE

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<220>  
 <221> unsure  
 <222> (2067)  
 <223> N AT POSITION 2067 INDICATES UNDETERMINED  
 NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2111)  
 <223> N AT POSITION 2111 INDICATES UNDETERMINED  
 NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2120)  
 <223> N AT POSITION 2120 INDICATES UNDETERMINED  
 NUCLEOTIDE

<400> 46

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cgtcagctc	gg	agcgcgcga	g	ccgcgtct	gaataagaag	tgagtacaat	ggcgtgtttg	120
taaaaaaaag	cttcaagttc	gt	cttttca	aaaacattt	tgaatgctgc	atgcctcatg	180	
cttccca	g	cctcgccgga	g	agacccggc	tatagagcag	gagtggcggc	acctgacttg	240
ctggatccta	aat	ctgcgcgc	tc	agaactcc	aaaccgaggc	tctcattttc	cacgaaaccc	300
acagtgc	ttt	cccgggt	gg	agagtgac	acgaccatta	atgttatgaa	atggaagacg	360
gtctccacga	tatt	cctgtgtt	gg	tgcgtctc	tatctgatca	tcggagccac	cgtgttcaaa	420
gcattggagc	ag	cctcatga	gatt	tcacag	aggaccacca	ttgtgatcca	gaagcaaaca	480
ttcatatccc	aa	cattcctg	tgt	caattcg	acggagctgg	atgaactcat	tcagcaaata	540
gtggcagcaa	taa	atgcagg	gatt	atacccg	ttaggaaaaca	cctccaatca	aatcagtcac	600
tgggatttgg	ga	agtttcctt	ctt	cttgcgt	ggcactgtt	ttacaaccat	aggatttgg	660
aacatctcac	cac	gcacaga	agg	ccggcaaa	atattctgt	tcatctatgc	cttacttgg	720
atccccctct	ttg	gttttct	ctt	ggctgg	gttggagatc	agctaggcac	catatttgg	780
aaaggaaattt	c	aaagtgg	agat	acgttt	attaagtgg	attttagtca	gaccaagatt	840
cgcacatcat	ca	acaatcat	attt	ataacta	tttggctgt	tactcttgc	ggctctgcct	900
gcatcatat	tca	aaacacat	aga	aggctgg	agtggccctgg	acggcattta	ttttgtgg	960
atca	ctt	caacttgg	at	tttgc	tacgttgcag	gtggatccga	tattgaat	1020
ctggacttct	at	aaaggctgt	cgt	gttgc	tggatcctt	tagggcttgc	ttactttgct	1080
gctgtcctga	gc	atgtgatttgc	gag	tttgc	cgagtgtat	ctaaaaagac	aaaagaagag	1140
gtgggagagt	tca	gagacaca	cg	ctgtctg	tggacagcca	acgtcacagc	cgaattcaaa	1200
gaaaccagga	gg	gcactgag	tgt	ggat	tatgacaagt	tccagcgggc	cacccatc	1260
aagcggaa	tct	ccggcaga	act	ggctgg	aaccacaatc	aggagctgac	tcctttagg	1320
aggaccctgt	c	agtgaacca	c	ctgaccagc	gagagggat	tcttcctcc	tttacttgaag	1380
actgagagta	tct	atctgtt	tgt	tttgc	ccacactgt	ctggtaaga	gattgtgt	1440
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ggggaa	aa	aatagata	cc	ccatcatgg	tcatctatca	tcaagagaat	tttgaattct	1620
gagccagcac	ttt	cttcttctg	at	gtatgc	ttgaacgccc	cacccat	gtgagtg	1680
atgacaagca	at	gtctgtat	cc	ttgtgt	cccagactgt	tttccctct	cttccctaa	1740
tgtgcataa	gg	ccctcaga	tga	atttgc	attgtttctg	gtaacaatgt	agctttgagg	1800
gatcagtct	ta	acttttca	gg	gttctac	aactgagcc	agatatggac	catttatgg	1860
tgacaacaat	ttt	tttttttgc	taa	atgc	aaaattctt	tgcagcc	tacctaagaa	1920
atttctgtca	gt	cccttatac	tt	atgc	acagaaccc	tctagctaat	gtgtgg	1980
tccttcctg	cccc	ccccacccc	tag	tcacc	tctgcagtt	tttacccag	tttcccatt	2040
tgaataccat	ac	cttgcgttgg	aa	acagngt	taaaatgact	gaagtgtat	tgccgaagat	2100
gaaatagatg	nc	aaatttagn	tgg	acattga				2130

<210> 47  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 aaaagatcta aaatgcttcc cagcgcc

27

<210> 48  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 aaagtcgacc tatttgatgt tctcaat

27

<210> 49  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 aaaaagctta aaatgcttcc cagcgcc

27

<210> 50  
 <211> 27  
 <212> DNA  
 <213> Homo sapiens

<400> 50  
 aaatctagac tatttgatgt tctcaat

27

<210> 51  
 <211> 534  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (262)  
 <223> N AT POSITION 262 INDICATES UNDETERMINED  
 NUCLEOTIDE

<400> 51  
 aacaaaaacc tttttgttt tgaatggcct agagaggta agggatcccc tgacgaacag 60  
 gagcagagcc agctagaacc tggcctggc cagttcaagg ccaccagagg gcagccttct 120  
 gcggaaggca gtattgggtt aggcaggac cccagcagac atggcactca gagctctcac 180  
 tgtccactga ctctctcttc tccaggttat ggccacatgg ccccaactatc gccaggcgga 240  
 aaggccttct gcatggtctt antagccctt gggctgccag cctccttagc tctcgtggcc 300  
 accctgcgcc attgcctgtc gcctgtgctc agcccccac gtgcctgggt agcggtccac 360  
 tggcagctgt caccggccag ggctgcgtc ctgcaggcag ttgcactggg actgctgggt 420  
 gccagcagct ttgtgctgtc gccagcgtc gtgcgtgtgg gccttcaggg cgactgcagc 480  
 ctgctggggg ccgtctactt ctgcttcagc tcgctcagca ccattggcct gggg 534

<210> 52  
 <211> 956  
 <212> DNA

&lt;213&gt; Mus musculus

<400> 52

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gcccgcgt	gttcgcgcga	ctggagtcgg	agccggagat	gatcgagcgg	cagcggctgg	180
agctgcggca	gctggagctg	cggcgcgcgt	acaacctcag	cgagggcggc	tacgaggagc	240
tggagcgcgt	cgtgcgtcgc	ctcaagccgc	acaaggccgg	cgtgcagtgg	cgcttcgcgg	300
gctccctcta	tttcgcgcatt	accgtcatca	ccaccatcg	ctatggtcat	gcggcgcccc	360
gcacgacgg	aggcaagggtg	ttctgcatgt	tctacgcgt	gctgggcattc	ccgctcacac	420
tagtcatgtt	ccagagccgt	ggtgaacgc	tcaacaccc	cgtgaggtac	ctgctgcacc	480
gtgccaagag	ggggctgggc	atgcggcgc	ccgaagtgtc	catggcaac	atgggtgtca	540
tcggtttgcgt	gtcgtgcattc	agcacgcgt	gcacgcgc	agctgccttc	tcctactacg	600
agcgctggac	tttcttccag	gcctattact	actgcttcat	caccctcacc	accatcggt	660
tcggcacta	tgtggcgctg	cagaaggacc	aggcgctgca	gacgcagccg	cagtatgtgg	720
cttcagcttc	gtgtacatcc	tcacgggctc	acggtcatcg	gcgccttc	aacctcgtgg	780
tgctgcgatt	catgaccatg	aacgcccagg	acgagaagcg	tgtatgcggag	caccgcgc	840
tgctcagcga	caacggccag	gctgtcgcc	tgggtggct	gagctgcctg	agcggtagcc	900
tggcgacgg	cgtgcgtccc	cgcgaccagg	tcacatgcgc	tgccgcgcga	agctta	956

&lt;210&gt; 53

&lt;211&gt; 1055

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (247)

&lt;223&gt; N AT POSITION 247 INDICATES UNDETERMINED NUCLEOTIDE

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (593)

&lt;223&gt; N AT POSITION 593 INDICATES UNDETERMINED NUCLEOTIDE

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (952)

&lt;223&gt; N AT POSITION 952 INDICATES UNDETERMINED NUCLEOTIDE

&lt;400&gt; 53

ctgaaaccat	gggcccata	cctgctcctg	cttatggccc	acctgctggc	catggccctt	60
ggggctgtgg	tgcttcagtc	cctggaggcc	cctccagctc	gccacccatc	ggcccaggcc	120
caggctgaac	tggcttagctt	ccaggcagag	cacagggcc	gcttgcacc	tgaggccctg	180
gaggagctgc	taggtgcgtt	cctgagagca	caggccatg	gagttccag	cctggcaac	240
agctcanaga	caagcaactg	ggatctgccc	tcagctctgc	tgttcactgc	cagcatcc	300
accaccaccg	gttatggcca	catggccca	ctctcctc	gtggaaaggc	cttctgtgt	360
gtctatgcag	cccttgggt	gccagccct	ctagcaccc	tggctgcct	gcgcactgc	420
ttgctgcctg	tgttcagtc	cccaggtgac	tgggttagcca	ttcgctggca	gctggcacca	480
gctcaggctg	ctctgctaca	ggcagcagga	ctgggcctcc	tggccctg	tgtcttcatg	540
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cgtggcctgc	accacgccc	ttaccaccc	ggcagtttgc	cacttcttgg	ttacttgcctc	720
ctggggctcc	tggccatgtt	gttagcagta	gagacccat	cagactgccc	tcaggccgt	780
gccatggta	aattttttgg	gcccaatggc	tctagaacc	atgaagatca	agatggccatc	840
ctagggcaag	atgagctg	tctgagact	gtgtgcctg	acggccca	cttgggacca	900
accacccag	cctgagcggg	aggcaccagg	gagtgcctg	agaacatagc	angaagggtt	960
atggaaatga	atatgtcatg	ggataatgtt	aattttaaaa	attaaatggg	ctgcttagca	1020
tgcaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaa			1055

<210> 54  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

---

<220>  
 <221> UNSURE  
 <222> (88)  
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

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 20 25 30  
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
 35 40 45  
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
 50 55 60  
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
 65 70 75 80  
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
 85 90 95  
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
 100 105 110  
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
 115 120 125  
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
 130 135 140  
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
 145 150 155 160  
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
 165 170 175  
 Leu Gly

<210> 55  
 <211> 309  
 <212> PRT  
 <213> Mus musculus

<400> 55  
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
 1 5 10 15  
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
 20 25 30  
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln

35

40

45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
 50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
 65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
 85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
 100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
 115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
 130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
 145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
 165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Phe Ser Tyr Tyr Glu Arg  
 180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
 195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
 210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
 225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
 245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
 260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser  
 275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala  
 290 295 300

Ala Ala Ala Ser Leu  
 305

<210> 56

<211> 304

<212> PRT

<213> Mus musculus

<220>

<221> UNSURE

<222> (83)

<223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (198)

&lt;223&gt; N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

&lt;400&gt; 56

Leu	Lys	Pro	Trp	Ala	Arg	Tyr	Leu	Leu	Leu	Leu	Met	Ala	His	Leu	Leu
1				5			10						15		
Ala	Met	Gly	Leu	Gly	Ala	Val	Val	Leu	Gln	Ala	Leu	Glu	Gly	Pro	Pro
			20				25					30			
Ala	Arg	His	Leu	Gln	Ala	Gln	Val	Gln	Ala	Glu	Leu	Ala	Ser	Phe	Gln
		35				40					45				
Ala	Glu	His	Arg	Ala	Cys	Leu	Pro	Pro	Glu	Ala	Leu	Glu	Glu	Leu	Leu
		50				55					60				
Gly	Ala	Val	Leu	Arg	Ala	Gln	Ala	His	Gly	Val	Ser	Ser	Leu	Gly	Asn
		65				70				75				80	
Ser	Ser	Xaa	Thr	Ser	Asn	Trp	Asp	Leu	Pro	Ser	Ala	Leu	Leu	Phe	Thr
			85					90					95		
Ala	Ser	Ile	Leu	Thr	Thr	Thr	Gly	Tyr	Gly	His	Met	Ala	Pro	Leu	Ser
		100				105					110				
Ser	Gly	Gly	Lys	Ala	Phe	Cys	Val	Val	Tyr	Ala	Ala	Leu	Gly	Leu	Pro
		115				120					125				
Ala	Ser	Leu	Ala	Leu	Val	Ala	Ala	Leu	Arg	His	Cys	Leu	Leu	Pro	Val
		130				135					140				
Phe	Ser	Arg	Pro	Gly	Asp	Trp	Val	Ala	Ile	Arg	Trp	Gln	Leu	Ala	Pro
		145				150				155			160		
Ala	Gln	Ala	Ala	Leu	Leu	Gln	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Val	Ala
			165				170					175			
Cys	Val	Phe	Met	Leu	Leu	Pro	Ala	Leu	Val	Leu	Trp	Gly	Val	Gln	Gly
			180				185					190			
Asp	Trp	Gln	Pro	Ala	Xaa	Thr	Ile	Tyr	Phe	Cys	Phe	Gly	Ser	Leu	Ser
		195					200					205			
Thr	Ile	Gly	Leu	Gly	Asp	Leu	Leu	Pro	Ala	His	Gly	Arg	Gly	Leu	His
		210				215					220				
Pro	Ala	Ile	Tyr	His	Leu	Gly	Gln	Phe	Ala	Leu	Leu	Gly	Tyr	Leu	Leu
		225				230				235			240		
Leu	Gly	Leu	Leu	Ala	Met	Leu	Leu	Ala	Val	Glu	Thr	Phe	Ser	Glu	Leu
			245				250					255			
Pro	Gln	Val	Arg	Ala	Met	Val	Lys	Phe	Phe	Gly	Pro	Ser	Gly	Ser	Arg
		260					265					270			
Thr	Asp	Glu	Asp	Gln	Asp	Gly	Ile	Leu	Gly	Gln	Asp	Glu	Leu	Ala	Leu
		275				280					285				
Ser	Thr	Val	Leu	Pro	Asp	Ala	Pro	Val	Leu	Gly	Pro	Thr	Thr	Pro	Ala
		290				295					300				

<210> 57

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (1)..(9)

<223> X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8 IS Y, F, V, I, M, OR L

<220>

<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<400> 57

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly  
1 5

<210> 58

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(8)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A, S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I, V, L, F, OR Y

<400> 58

Xaa Xaa Xaa Xaa Gly Xaa Pro Xaa  
1 5

<210> 59

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

<400> 59

Tyr Ala Leu Leu Gly Ile Pro  
1 5

<210> 60

<211> 7

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: POTASSIUM ION  
 CHANNEL SEQUENCE

<220>  
 <221> VARIANT  
 <222> (6)  
 <223> X AT POSITION 6 IS M, I, V, L, F, OR Y

<400> 60  
 Tyr Ala Leu Leu Gly Xaa Pro  
 1 5

<210> 61  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
 <222> (88)  
 <223> X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

<400> 61  
 Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser  
 1 5 10 15  
 Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe  
 20 25 30  
 Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
 35 40 45  
 Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
 50 55 60  
 Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
 65 70 75 80  
 Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
 85 90 95  
 Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
 100 105 110  
 Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
 115 120 125  
 Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
 130 135 140  
 Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
 145 150 155 160  
 Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
 165 170 175  
 Leu Gly

<210> 62  
 <211> 309  
 <212> PRT  
 <213> Mus musculus

<400> 62  
 Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
 1 5 10 15  
 Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
 20 25 30  
 Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln  
 35 40 45  
 Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
 50 55 60  
 Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
 65 70 75 80  
 His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
 85 90 95  
 Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
 100 105 110  
 Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
 115 120 125  
 Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
 130 135 140  
 Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
 145 150 155 160  
 Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
 165 170 175  
 Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
 180 185 190  
 Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
 195 200 205  
 Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
 210 215 220  
 Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
 225 230 235 240  
 His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
 245 250 255  
 Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
 260 265 270  
 Thr His Asn Gly Gln Ala Val Gly Leu Gly Leu Ser Cys Leu Ser  
 275 280 285  
 Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala

Ala Ala Ala Ser Leu  
305

<210> 63

<211> 434

<212> PRT

<213> *Caenorhabditis elegans*

<400> 63

Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala Val Glu Gln Glu Ala  
1 5 10 15

Phe Pro Arg Asp Lys Tyr Asn Ile Val Tyr Trp Leu Val Ile Leu Val  
20 25 30

Gly Phe Gly Val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro  
35 40 45

Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp  
50 55 60

Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro  
65 70 75 80

Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro  
85 90 95

Leu Ile Tyr Arg Val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu  
100 105 110

Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser  
115 120 125

Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn  
130 135 140

Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly Val Gly Gly Asp  
145 150 155 160

Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys  
165 170 175

Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn  
180 185 190

Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val  
195 200 205

Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp  
210 215 220

Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala  
225 230 235 240

Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn  
245 250 255

Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu  
260 265 270

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Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly  
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu  
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val  
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile  
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn Tyr Arg  
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe  
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala  
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg  
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr  
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser  
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,  
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,  
L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro  
1 5

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence between Ce orf1 and Dm orf1

<400> 65  
Thr Trp Thr Phe  
1

-----  
<210> 66-----  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence between Ce orf1 and Dm orf1

<400> 66  
Gly Tyr Gly Asn  
1

<210> 67  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence between Ce orf1 and Dm orf1

<400> 67  
Gly Phe Gly Asp  
1